

1642

RAW SEQUENCE LISTIN

DATE: 05/02/2000

PATENT APPLICATION: US/09/274,752A

TIME: 08:36:36

Input Set : A:\A-67501.app

Output Set: N:\CRF3\050200\I274752A.raw

3 <110> APPLICANT: Goetzl, Edward L.
 4 An, Songzhu
 6 <120> TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipids and
 7 Sphingolipids and Nucleic Acids Encoding the Same
 9 <130> FILE REFERENCE: A-67501/DJB/TAL
 11 <140> CURRENT APPLICATION NUMBER: 09/274,752
 12 <141> CURRENT FILING DATE: 1999-03-23
 14 <160> NUMBER OF SEQ ID NOS: 29
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 382
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
 23 <400> SEQUENCE: 1
 24 Met Val Ile Met Gly Gln Cys Tyr Tyr Asn Glu Thr Ile Gly Phe Phe
 25 1 5 10 15
 27 Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
 28 20 25 30
 30 Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
 31 35 40 45
 33 Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
 34 50 55 60
 36 Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Asp Leu Phe
 37 65 70 75 80
 39 Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
 40 85 90 95
 42 Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
 43 100 105 110
 45 Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
 46 115 120 125
 48 Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
 49 130 135 140
 51 Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
 52 145 150 155 160
 54 Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
 55 165 170 175
 57 Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
 58 180 185 190
 60 Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
 61 195 200 205
 63 Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
 64 210 215 220
 66 His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
 67 225 230 235 240
 69 Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
 70 245 250 255
 72 Gly Gln Val Val Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn

Does Not Comply
 Corrected Diskette Needed

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73          260          265          270
75 Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
76          275          280          285
78 Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ser Glu Met Arg Arg
79          290          295          300
81 Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
82 305          310          315          320
84 Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
85          325          330          335
87 Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
88          340          345          350
90 Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
91          355          360          365
93 Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp
94          370          375          380
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98 <211> LENGTH: 1734
99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
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104 tctgcggcgt gactggaggc ccagatggtc atcatgggcc agtgctacta caacgagacc 120
105 atcggcttct tctataacaa cagtggcaaa gagctcagct ccactggcg gcccaaggat 180
106 gtggctcgtg tggcactggg gctgaccgtc agcgtgctgg tgcgtgctgac caatctgctg 240
107 gtcatagcag ccatcgcttc caaccgcgcg ttccaccagc ccacttacta cctgctcggc 300
108 aatctggccg cggtgacact cttcgcgggc gtggcctacc tcttcctcat gttccacact 360
109 ggtccccgca cagccccgact ttacttgag ggctggttcc tgcggcaggg cttgctggac 420
110 acaagcctca ctgcgtcggt ggccacactg ctggccatcg ccgtggagct gcaccgcagt 480
111 gtgatgtccg tgcagctgca cagccgcctg ccccgaggcc gcgtggatcat gtcattgtg 540
112 ggcgtgtggg tggtgcctt gggcctgggg ctgctgcctg cccactcctg gcaactgcctc 600
113 tgtgcccctg accgctgctc acgcatggca cccctgctca gccgctccta tttggccgtc 660
114 tgggctctgt cgagcctgtc tgtcttctg ctcatgggtg ctgtgtacac ccgcatttct 720
115 ttctacgtgc ggcggcgagt gcagcgcagt gcagagcatg tcagctgccca cccccgctac 780
116 cgagagacca cgctcagcct ggtcaagact gttgtcatca tcctgggggc gttcgtggtc 840
117 tgctggacac caggccaagg ggtactgctc ctggatgggt taggctgtga gtcctgcaat 900
118 gtcctggctg tagaaaagta cttcctactg ttggccgagg ccaactcact ggtcaatgct 960
119 gctgtgtact cttgccgaga tgcgtgagat gcgcgcacct tccgcgcctt tctctgctgc 1020
120 gcgtgcctcc gccagtcac ccgcgagtct gtccactata catcctctgc ccaggaggat 1080
121 gccagcactc gcatcatgct tcccagagaa ggccacccac tgatgactcc accctttagc 1140
122 taccttgaac ttcagcggtg gcgcgcaagc aacaaatcca cagccccctg tgacttgttg 1200
123 gtgctccttg ctcaacccaa ccaacaggac tgactgactg gcaggacaag gtcctggcatg 1260
124 gcacagcacc actgccaggc ctccccaggc acaccactct gccaggga tgggggcttt 1320
125 gggatcatct cactgcctg ggggagtcag atggggtgca ggaatctggc tcttcagcca 1380
126 tctcagggtt aggggggttg taacagacat tattctgttt tcaactgcgtg tccttggtta 1440
127 gccctgtgga ctgggttaatg ctgtgtgatg ctgagggttt taagggtggg agagataagg 1500
128 gctctctcgg gccatgtac ccggtatgac tgggtaatga ggacagactg tggacacccc 1560
129 atctacctga gtctgattct ttagcagcag agactgaggg gtgcagagtg tgagctggga 1620
130 aagggtttgt gtccttgca gcctccaggg actggcctgt ccccaataga attgaagcag 1680
131 tccacgggga ggggatgata caaggagtaa acctttcttt acactcaaaa aaaa 1734

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Input Set : A:\A-67501.app

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133 <210> SEQ ID NO: 3
134 <211> LENGTH: 353
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 3
139 Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
140 1 5 10 15
142 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
143 20 25 30
145 Arg Gln Val Ala Ser Ala Gly Ile Val Ile Leu Cys Cys Ala Ile Val
146 35 40 45
148 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
149 50 55 60
151 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
152 65 70 75 80
154 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
155 85 90 95
157 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
158 100 105 110
160 Ser Ile Thr Leu Ser Ala Ser Val Gly Ser Leu Leu Ala Ile Ala Ile
161 115 120 125
163 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Cys Lys
164 130 135 140
166 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
167 145 150 155 160
169 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
170 165 170 175
172 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
173 180 185 190
175 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
176 195 200 205
178 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
179 210 215 220
181 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
182 225 230 235 240
184 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
185 245 250 255
187 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
188 260 265 270
190 Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
191 275 280 285
193 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
194 290 295 300
196 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr
197 305 310 315 320
199 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
200 325 330 335
202 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
203 340 345 350

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MAY 09 2000
TECH CENTER 1600/2900

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Input Set : A:\A-67501.app

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205 Val
209 <210> SEQ ID NO: 4
210 <211> LENGTH: 1122
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 4
215 atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat 60
216 accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcac 120
217 gtcatcctct gttgcgccat gcaggagacg acctcccgcc aggtggcctc ggccttcac 180
218 gtcatcctct gttgcgccat tgtggtggaa aaccttctgg tgctcattgc ggtggcccga 240
219 aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta 300
220 ctggcaggcg tggccttcgt agccaatadd ttgctctctg gctctgtcac gctgaggctg 360
221 acgctgtgac agtggtttgc ccgggagggc tctgcctcca tcacgctctc ggcctctgtc 420
222 ttcagcctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggt caagctgtat 480
223 ggcagcgaca agagctgccc catgcttctg ctcatcgggg cctcgtggct catctcgctg 540
224 gtcctcggtg gcctgcccac ccttggtctg aactgcttgg gccacctoga ggcctgtctc 600
225 actgtcctgc ctctctacgc caagcattat gtgctgtgcg tggtgaccat cttctccatc 660
226 atcctgttgg ccacgtgggc cctgtacgtg cgcatctact gcgtggtccg ctcaagccac 720
227 gctgacatgg ccgccccgca gacgctagcc ctgctcaaga cggtcaccat cgtgctaggg 780
228 gtctttatcg tctgttggct gcccgccctc agcatcctcc ttctggacta tgcctgtccc 840
229 gtccactcct gcccgatcct ctacaaagcc cactactttt tcgccgtctc caccctgaat 900
230 tccctgtctc acccgcgtat ctacacgtgg cgcagccggg acctgcggcg ggaggtgctt 960
231 cggccgctgc agtgctggcg gccgggggtg ggggtgcaag gacggaggcg ggtcggggac 1020
232 ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1080
233 cccacgtcac ccacgtttct ggagggcaac acggtgtgtc ga 1122
235 <210> SEQ ID NO: 5
236 <211> LENGTH: 375
237 <212> TYPE: DNA
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 5
241 gggccatggc tcgagccgcc ccgacccccg gcgagccgcg cttgtctgcg gcgtgactgg 60
242 agggccagat ggtcatcatg ggccagtgtc actacaacga gaccatcggc ttctctata 120
243 acaacagtgg caaagagctc agctccactt ggccggccaa ggatgtggtc gtggtggcac 180
244 tggggctgac cgtcagcgtg ctggtgctgc tgaccaatct gctggtcata gcagccatcg 240
245 cctccaaccg ccgcttcac cagcccatct actacctgct cggaatctg gccgaggctg 300
246 acctcttcgc gggcgtggct acctcttct catgttcac actggtcccc gcacagcccg 360
247 actttcactt gaggg 375
249 <210> SEQ ID NO: 6
250 <211> LENGTH: 8
251 <212> TYPE: PRT
252 <213> ORGANISM: combination of rat and human.
254 <400> SEQUENCE: 6
255 Leu Leu Ala Ile Ala Ile Glu Arg
256 1
259 <210> SEQ ID NO: 7
260 <211> LENGTH: 22
261 <212> TYPE: DNA
262 <213> ORGANISM: combination of rat and human.
264 <220> FEATURE:

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Input Set : A:\A-67501.app

Output Set: N:\CRF3\050200\I274752A.raw

265 <221> NAME/KEY: misc_feature
 266 <222> LOCATION: (6)
 267 <223> OTHER INFORMATION: The n at position 6 can be g or c.
 269 <220> FEATURE:
 270 <221> NAME/KEY: misc_feature
 271 <222> LOCATION: (12)
 272 <223> OTHER INFORMATION: The n at position 12 can be c or t.
 274 <220> FEATURE:
 275 <221> NAME/KEY: misc_feature
 276 <222> LOCATION: (17)
 277 <223> OTHER INFORMATION: The n at position 17 can be c or t.
 279 <220> FEATURE:
 280 <221> NAME/KEY: misc_feature
 281 <222> LOCATION: (21)
 282 <223> OTHER INFORMATION: The n at position 21 can be a or c.
 284 <400> SEQUENCE: 7
 W--> 285 ~~ctcctngcca tngcatngag ng~~ 22
 287 <210> SEQ ID NO: 8
 288 <211> LENGTH: 8
 289 <212> TYPE: PRT
 290 <213> ORGANISM: combination of rat and human.
 292 <400> SEQUENCE: 8
 293 Leu Leu Leu Leu Asp Ser Thr Cys
 294 1 5
 297 <210> SEQ ID NO: 9
 298 <211> LENGTH: 22
 299 <212> TYPE: DNA
 300 <213> ORGANISM: combination of rat and human.
 302 <220> FEATURE:
 303 <221> NAME/KEY: misc_feature
 304 <222> LOCATION: (4)
 305 <223> OTHER INFORMATION: The n at position 4, 16 and 22 can be c or g.
 307 <220> FEATURE:
 308 <221> NAME/KEY: misc_feature
 309 <222> LOCATION: (6)
 310 <223> OTHER INFORMATION: The n at position 6 and 8 can be a or c.
 312 <220> FEATURE:
 313 <221> NAME/KEY: misc_feature
 314 <222> LOCATION: (7)
 315 <223> OTHER INFORMATION: The n at position 7, 9, and 19 can be a or g.
 317 <400> SEQUENCE: 9
 W--> 318 ~~cagttttttt ccagttttttt na~~ 22
 320 <210> SEQ ID NO: 10
 321 <211> LENGTH: 24
 322 <212> TYPE: DNA
 323 <213> ORGANISM: Homo sapiens
 325 <400> SEQUENCE: 10
 326 gcaggacagt ggagcaggcc tcga 24
 328 <210> SEQ ID NO: 11

what about n at location 15, 18, and 21?

a is at locations 16 and 22

a is at location 19

VERIFICATION SUMMARY

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Output Set: **N:\CRF3\050200\I274752A.raw**

L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9